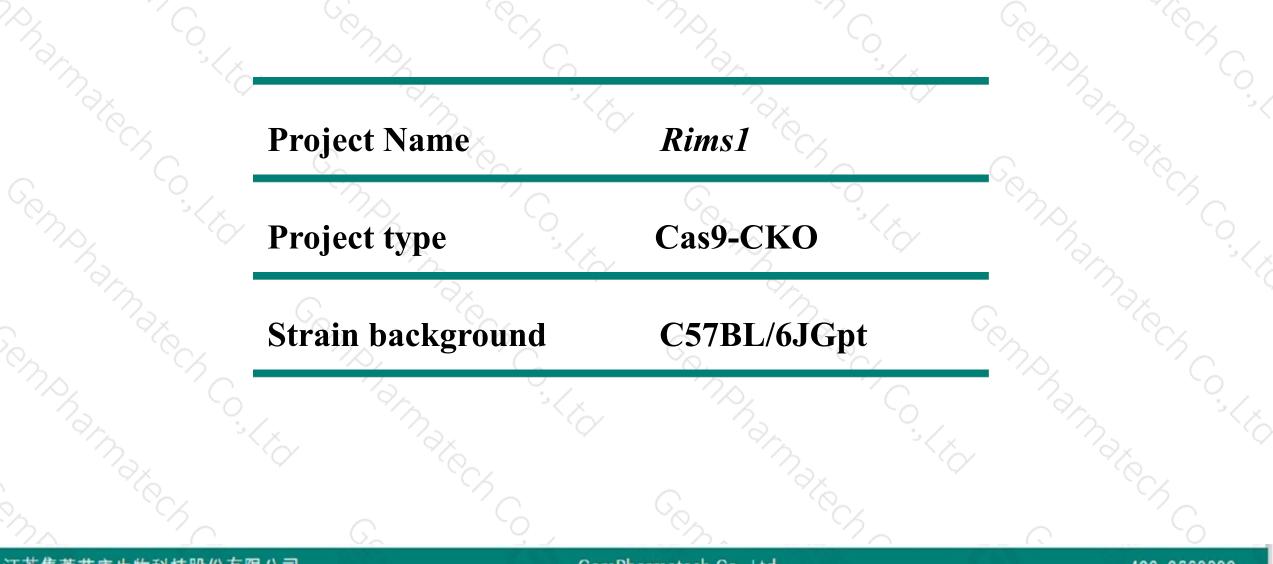


# **Rims1** Cas9-CKO Strategy

Designer: Reviewer: Design Date: Huimin Su Ruirui Zhang 2020/2/12

# **Project Overview**





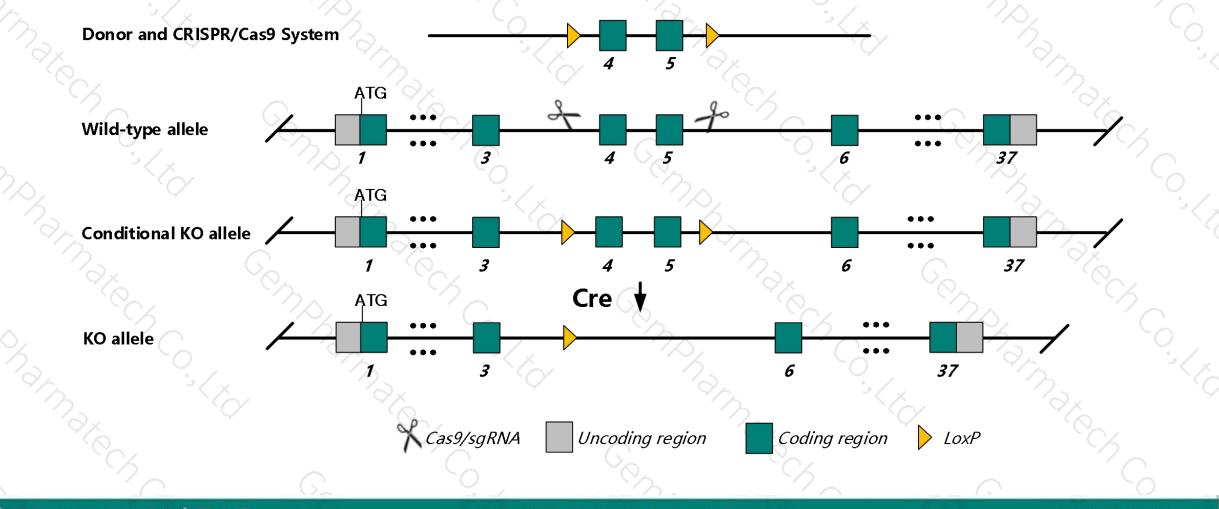
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## **Conditional Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Rims1* gene. The schematic diagram is as follows:



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The Rims1 gene has 11 transcripts. According to the structure of Rims1 gene, exon4-exon5 of Rims1-205 (ENSMUST00000097811.9) transcript is recommended as the knockout region. The region contains 226bp of coding reigon. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rims1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- According to the existing MGI data, Mice homozygous for disruptions in this gene display defects in maternal care and abnormalities in synaptic transmission in the central nervous system.
- > Rims1-207, Rims1-208 and Rims1-210 transcripts are incomplete, so the effect on them are unknown.
- The *Rims1* gene is located on the Chr1. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# **Gene information (NCBI)**

21398399

Kcnq5

Gm7658



☆ ?

Rims1 regulating synaptic membrane exocytosis 1 [ Mus musculus (house mouse) ]

Gene ID: 116837, updated on 13-Jan-2020

Summary

Official Symbol Rims1 provided by MGI Official Full Name regulating synaptic membrane exocytosis 1 provided by MGI Primary source MGI:MGI:2152971 Ensembl:ENSMUSG0000041670 See related Gene type protein coding RefSeq status VALIDATED Organism Mus musculus Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus Also known as Rim; RIM1; RIM1a; Serg1; Rab3ip1; RIM1alpha; C030033M19Rik Annotation information Annotation category: partial on reference assembly Expression Biased expression in cortex adult (RPKM 23.6), frontal lobe adult (RPKM 17.0) and 5 other tissues See more Orthologs human all

Chromosome 1 - NC\_000067.6

Gm5696 🚽

Rims1 +

22986554

Gm7761

Gm7759

# **Transcript information (Ensembl)**



#### The gene has 11 transcripts, all transcripts are shown below:

Name 🖕 Transcript ID 🖕 b		bp 👌	Protein 🖕	Biotype 🍦	CCDS 🍦	UniProt 🖕	Flags		
Rims1-205	ENSMUST0000097811.9	6446	<u>1424aa</u>	Protein coding	376S	F6VBR4 密	TSL:5 GENCODE basic APPRIS P5		
Rims1-204	ENSMUST0000097810.9	6362	<u>1396aa</u>	Protein coding	376 S	F6VBT9	TSL:5 GENCODE basic APPRIS ALT2		
Rims1-203	ENSMUST0000097809.9	6179	<u>1335aa</u>	Protein coding	576S	<u>F6VBV0</u> &	TSL:5 GENCODE basic APPRIS ALT2		
Rims1-206	ENSMUST00000115273.8	6107	<u>1311aa</u>	Protein coding	558S	<u>F6Y0S3</u> 교	TSL:5 GENCODE basic APPRIS ALT2		
Rims1-201	ENSMUST0000081544.12	5954	<u>1260aa</u>	Protein coding	558S	F6TZK4	TSL:5 GENCODE basic APPRIS ALT2		
Rims1-202	ENSMUST0000097808.6	2411	<u>803aa</u>	Protein coding	356S	E9PWP6 &	CDS 3' incomplete TSL:5		
Rims1-207	ENSMUST00000164877.7	2294	<u>219aa</u>	Protein coding	356S	Q7TPL9&	TSL:1 GENCODE basic		
Rims1-208	ENSMUST00000185942.1	2189	<u>729aa</u>	Protein coding	\$56S	A0A087WSA4 @	CDS 5' incomplete TSL 1		
Rims1-209	ENSMUST00000218140.1	1434	<u>388aa</u>	Protein coding	556S	<u>A0A1W2P6S9</u> &	TSL:5 GENCODE basic		
Rims1-210	ENSMUST00000239255.1	516	<u>129aa</u>	Protein coding	\$765	15-201	CDS 3' incomplete		
Rims1-211	ENSMUST00000239339.1	863	No protein	Processed transcript	1000	1876			

The strategy is based on the design of Rims1-205 transcript, The transcription is shown below

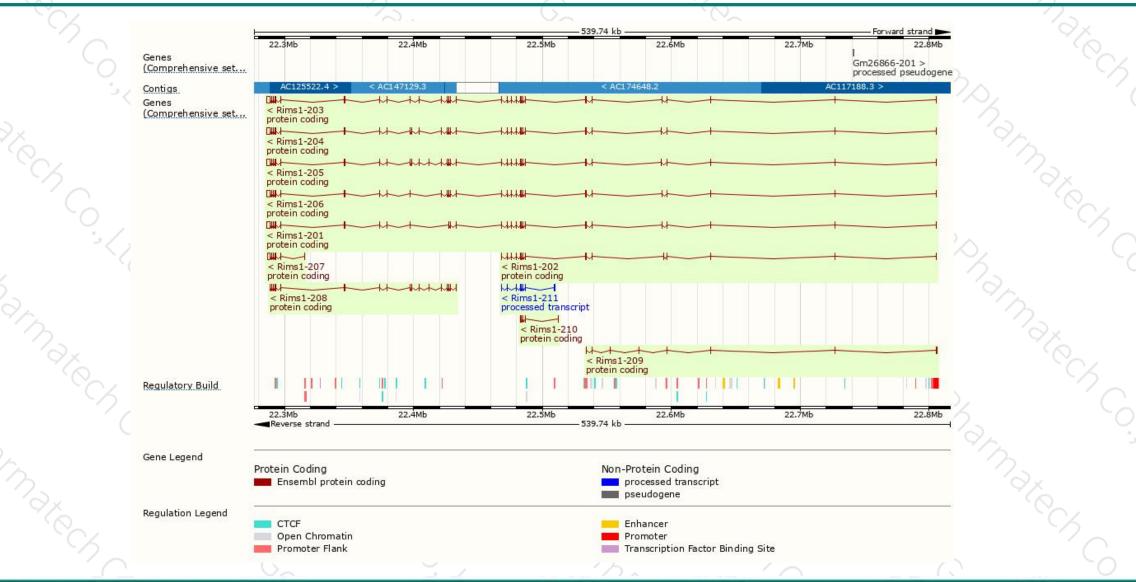
< Rims1-205 protein coding

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### **Genomic location distribution**





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# **Protein domain**



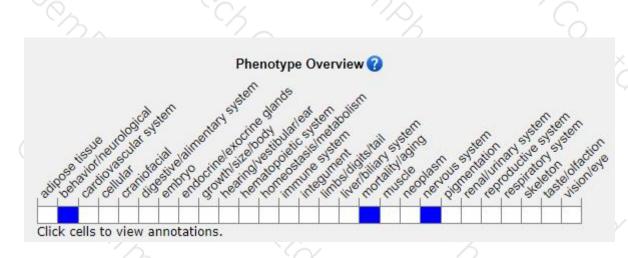
	$\sim$					C C		
	ENSMUSP00000095 MobiDB lite Low complexity (Seg) Coiled-coils (Ncoils) Superfamily	Zinc finger, FYVE/PHD-type	PDZ superfamily	SSF49 562			·	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
S.	SMART. Pfam.	FYVE-type zinc f	PDZ domain					, e S
	PROSITE profiles	Rab-binding domain	PDZ domain				C2 domain	~~~
	PANTHER	Zinc finger, FYV Rim-like						0./
3	Gene3D CDD	Regulating synaptic membrane	exocytosis protein 1 2.30.42.10 cd00992	C2 domain superfan	nily		04028	×
	All sequence SNPs/i	Sequence variants (dbSNP a	nd all other sources)	ų	$\mathbf{U}(\mathbf{t})$	10.1 1.001 01 0110	0	`ЧС
	Variant Legend	stop gained			inframe insertion			
	یک چ				13Mmax		nay.	
	°%	G_	°C _	Gen.		3	0	~^ ~

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# Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

Mice homozygous for disruptions in this gene display defects in maternal care and abnormalities in synaptic transmission in the central nervous system.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



